

Appl. No. 10/647,268
Amdt. Dated August 16, 2005
Reply to Office Action of May 24, 2005

IN THE SPECIFICATION

Replace Paragraph [0031] with the following:

[0031] FIG. 6 shows a comparison of the deduced amino acid sequences of *Sbul1* (SEQ ID NO:4), which confers late blight resistance in transgenic plants, and *Sbul2* (SEQ ID NO:6) which does not. Comparison reveals 101 differences between the two proteins over 989 residues, or 90% identity.

Replace Paragraph [0032] with the following:

[0032] FIG. 7 shows a comparison of the nucleic acid sequences of *Sbul1* (SEQ ID NO:4), which confers late blight resistance in transgenic plants, and *Sbul2* (SEQ ID NO:6) which does not. Comparison reveals 221 differences between the two genes over 3174 bp of coding sequence, or 93% identity.

Replace Paragraph [0046] with the following:

[0046] The present invention is directed to isolated nucleic acid sequences derived from a *S. bulbocastanum* gene which encode polypeptides which confer horizontal late blight resistance. The specifically exemplified nucleic acid sequences include the *Sbul1* cDNA sequence (SEQ ID NO:1) and the DNA sequence of the active *Sbul1* gene, a PCR product using template DNA from a late blight-resistant back cross 3 potato line containing *S. bulbocastanum* DNA (SEQ ID NO:3). The latter sequence contains a 412 bp intron. SEQ ID NO:4 shows the deduced amino acid sequence of the *Sbul1* gene product. The invention encompasses nucleic acid sequences which have greater than about 93% sequence identity with the coding domain of the exemplified sequences and encode a polypeptide which confers or enhances a plant's resistance to late blight. More preferably, the nucleic acid sequences have about 95% sequence identity with the coding domain of the exemplified sequences and encode a polypeptide which confers or

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enhances a plant's resistance to late blight. For purposes of the present invention, the degree of identity between two nucleic acid sequences is determined by any method known in the art, for example by the Clustal method (Thompson *et al.* 1994), using ClustalW 1.7 or 1.8 (<http://dot.imgen.bcm.tmc.edu:9331/multi-align/multi-align.html>). Further, nucleic acid sequences which hybridize under high stringency conditions with the coding region of the DNA sequence of SEQ ID NO:1 or 3 and which encode a polypeptide having the activity defined above, are also encompassed by the present invention.

Replace Paragraph [0047] with the following:

[0047] The invention is directed to nucleic acid molecules encoding the amino acid sequence of SEQ ID NO:4, or an amino acid sequence showing greater than about 90% sequence identity with SEQ ID NO:4 and which encodes a polypeptide having ability to confer or enhance a plant's resistance to late blight. More preferably, the encoded amino acid sequence has at least about 95%, and most preferably at least about 97% sequence identity with SEQ ID NO:4 and has the activity defined above. For purposes of the present invention, the degree of identity between two amino acids is determined by any method known in the art, for example, by the FASTA/FASTP method of Pearson (1990), using ALIGN (<http://dot.imgen.bcm.tmc.edu:9331/seq-search/alignment.html>), with the BLOSUM50 or PAM250 scoring matrix.